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10/699,024	10/31/2003	Jagir Razak Jainul Abdeen Hussan	JP920030152US1	2138

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Please find below and/or attached an Office communication concerning this application or proceeding.

The time period for reply, if any, is set in the attached communication.

-- *The MAILING DATE of this communication appears on the cover sheet with the correspondence address --*

Period for Reply

A SHORTENED STATUTORY PERIOD FOR REPLY IS SET TO EXPIRE _3_ MONTH(S) OR THIRTY (30) DAYS, WHICHEVER IS LONGER, FROM THE MAILING DATE OF THIS COMMUNICATION.
- Extensions of time may be available under the provisions of 37 CFR 1.136(a). In no event, however, may a reply be timely filed after SIX (6) MONTHS from the mailing date of this communication.
- If NO period for reply is specified above, the maximum statutory period will apply and will expire SIX (6) MONTHS from the mailing date of this communication.
- Failure to reply within the set or extended period for reply will, by statute, cause the application to become ABANDONED (35 U.S.C. § 133).
  Any reply received by the Office later than three months after the mailing date of this communication, even if timely filed, may reduce any earned patent term adjustment. See 37 CFR 1.704(b).

Status

1)☒ Responsive to communication(s) filed on _03 May 2010_.

2a)☒ This action is **FINAL**.   2b)☐ This action is non-final.

3)☐ Since this application is in condition for allowance except for formal matters, prosecution as to the merits is closed in accordance with the practice under *Ex parte Quayle*, 1935 C.D. 11, 453 O.G. 213.

Disposition of Claims

4)☒ Claim(s) _3-6,10,14-22 and 24-28_ is/are pending in the application.

    4a) Of the above claim(s) _____ is/are withdrawn from consideration.

5)☐ Claim(s) _____ is/are allowed.

6)☒ Claim(s) _3-6, 10, 14-22, 24-28_ is/are rejected.

7)☐ Claim(s) _____ is/are objected to.

8)☐ Claim(s) _____ are subject to restriction and/or election requirement.

Application Papers

9)☐ The specification is objected to by the Examiner.

10)☐ The drawing(s) filed on _____ is/are: a)☐ accepted or b)☐ objected to by the Examiner.

    Applicant may not request that any objection to the drawing(s) be held in abeyance. See 37 CFR 1.85(a).

    Replacement drawing sheet(s) including the correction is required if the drawing(s) is objected to. See 37 CFR 1.121(d).

11)☐ The oath or declaration is objected to by the Examiner. Note the attached Office Action or form PTO-152.

Priority under 35 U.S.C. § 119

12)☐ Acknowledgment is made of a claim for foreign priority under 35 U.S.C. § 119(a)-(d) or (f).

    a)☐ All b)☐ Some * c)☐ None of:

      1.☐ Certified copies of the priority documents have been received.

      2.☐ Certified copies of the priority documents have been received in Application No. _____.

      3.☐ Copies of the certified copies of the priority documents have been received in this National Stage application from the International Bureau (PCT Rule 17.2(a)).

    * See the attached detailed Office action for a list of the certified copies not received.

Attachment(s)

1)☐ Notice of References Cited (PTO-892)

2)☐ Notice of Draftsperson's Patent Drawing Review (PTO-948)

3)☐ Information Disclosure Statement(s) (PTO/SB/08) Paper No(s)/Mail Date _____.

4)☐ Interview Summary (PTO-413) Paper No(s)/Mail Date. _____

5)☐ Notice of Informal Patent Application

6)☐ Other: _____.

DETAILED ACTION

Status of Claims

Claims 3-6, 10, 14-22, 24-28 are pending and under consideration.

Claims 1-2, 7-9, 11-13, and 23 are cancelled.

Withdrawn Rejections

The rejection of claims 3-6, 10, 14-22, 24-28 under 35 U.S.C. 112, is withdrawn in view of applicant's amendments filed 05/03/2010.

Claim rejections - 35 USC § 112, 2nd Paragraph

The following is a quotation of the second paragraph of 35 U.S.C. 112:

> The specification shall conclude with one or more claims particularly pointing out and distinctly claiming the subject matter which the applicant regards as his invention.

Claims 3-6, 10, 14-22 are rejected under 35 U.S.C. 112, second paragraph, as being indefinite for failing to particularly point out and distinctly claim the subject matter which applicant regards as the invention. Claims that depend directly or indirectly from claim 14 are also rejected due to said dependence.

The following rejections are maintained.

Claims 14, 24, 27, and 28 (see step viii) recites a step for generating a first instance of a sequence "wherein generating of the sequence is responsive to…", "…and responsive to the …stored match-data entries", and "…the updating being responsive." In each case, the recitation of the limitation "responsive" renders the claims indefinite for

the following reasons. It is unclear in what way a computer system generates a representation of a sequence that is "responsive" to a stored backbone sequence and stored match-set data, for example. Similarly, it is unclear in what way updating is "being responsive" to the position. What active method steps are intended by the terms "responsive" and "being responsive"? Applicant's amendments have not clarified this issue and the specification provides no guidance. For purposes of examination, the term "responsive" is interpreted as meaning "includes"; e.g. generating of the sequence includes the stored backbone sequence.

Claims 14, 24, 27, and 28 (see step x) recites the limitation "generating...a second instance of the sequence to a user <u>responsive</u> to the at least second one of the replets." In each case, the recitation of the limitation "responsive" renders the claims indefinite for the following reasons. It is unclear in what way a computer system generates a representation of a sequence to a user "responsive" to a stored backbone sequence and stored match-set data. What active method step is intended by the term "responsive"? Applicant's amendments have not clarified this issue and the specification provides no guidance. For purposes of examination, the term "responsive" is interpreted as meaning "including."

Claim Rejections - 35 USC § 103

The following is a quotation of 35 U.S.C. 103(a) which forms the basis for all obviousness rejections set forth in this Office action:

(a) A patent may not be obtained though the invention is not identically disclosed or described as set forth in section 102 of this title, if the differences between the subject matter sought to be patented and the prior art are such that the subject matter as a whole would have been obvious at the time the invention was made to a person

having ordinary skill in the art to which said subject matter pertains. Patentability shall not be negatived by the manner in which the invention was made.

This application currently names joint inventors. In considering patentability of the claims under 35 U.S.C. 103(a), the examiner presumes that the subject matter of the various claims was commonly owned at the time any inventions covered therein were made absent any evidence to the contrary. Applicant is advised of the obligation under 37 CFR 1.56 to point out the inventor and invention dates of each claim that was not commonly owned at the time a later invention was made in order for the examiner to consider the applicability of 35 U.S.C. 103(c) and potential 35 U.S.C. 102(e), (f) or (g) prior art under 35 U.S.C. 103(a).

Claims 4, 5, 14-22, 24, 27, and 28 are rejected under 35 U.S.C. 103(a) as being unpatentable over Rigoutsos et al. (Bioinformatics, 1998, Vol. 14, No. 1, p. 55-67), in view of Chen et al. (Bioinformatics, 2002, Vol. 18, No. 12, p.1696-1698), in view of Orcutt et al. (Nucleic Acids Research, 1982, Vol. 10, No. 1, p. 157-174), in view of Zhang et al. (Genome Research, 1997, Vol. 7, p.649-656), and in view of UK CROPNETT (http://ukcrop.net/agr/sequence_display_key#sequence; Published 2001, p.1-5).

The following rejection is maintained but has been modified to address new limitations in the claims, as necessitated by applicant's amendment filed 05/03/2010.

The amended claims are now drawn to a computer system-implemented method for storing and presenting sequence data. Critical limitations of claims 1, 24, and 27 include specifying a set of replets for analysis by a computer system; ii) for each replet in the set, comparing each replet by the computer system to a sequence for determining by the computer system a subsequence of the sequence that matches each replet, if any, wherein the sequence represents a genome sequence; iii) generating by the computer

system responsive to the comparing, respective entries of a match-set data structure, the match-set data structure having respective entries for the each-respective replets, each entry comprising a sequence identification to identify a subsequence where a match occurs and offset information to determine a position within the sequence where the matching subsequence of the sequence is located, wherein the offset information comprises a first and second position parameter, iv) storing the generated entries of the match-set data structures in a computer readable memory by the computer system; v) deleting by the computer system each matching subsequence from the sequence where it is found; vi) concatenating by the computer system, in order, unmatched regions of sequences that remain after deleting each matching subsequence to form and store a backbone sequence; vii) the computer system generating or receiving a selection of at least a first one of the replets, wherein at least a portion of one of the matching subsequences is matched by a certain plurality of the replets and the received selection includes a selection of at least one of the certain plurality of replets; viii) the computer system generating a first instance of the sequence and presenting the first instance of the sequence to a user of the computer system, wherein the generating of the sequence is responsive to the stored backbone sequence and responsive to the at least one of the stored match-set data entries corresponding to the selected at least first one of the replets, wherein the first position parameter of each match-set data structure entry denotes a location in the sequence and the second position parameter of each match- set data structure entry denotes an offset from the location, wherein the selected at least first one of the replets has a position within the sequence, and wherein after receiving the selection the computer system updates the first and second parameters of the entries in the match-

set data structure the updating being responsive to the position of the selected at least first one of the replets; ix) the computer system generating or receiving a selection of a second one of the replets and x) the computer system generating or receiving a selection of a second one of the replets and x) the computer system generating and presenting a second instance of the sequence to a user responsive to at least second one of the replets and wherein the computer system performs the generating of the second instance of the sequence by reference to the updated first and second parameters for the second one of the replets. It is noted that the specification defines replets to be patterns used to represent sequences [p.7].

Rigoutsos teaches a computer-based program (i.e. TEIRESIAS) for discovering biological sequences [Abstract and p.56]. In particular, the program generates patterns entries representing a sequence [See Table 2], which meets claim language for specifying a set of replets in view of applicant's Remarks filed 11/04/2009 [page 7]. The program compares each pattern (i.e. replete) to a sequence for determining a subsequence, and generates entries of match-set data structures. Notation is provided for identifying generated patterns with their associated sequence identification data and offset information [Fig. 1, and p.56, Col. 2], which shows match-set data having respective entries comprising sequence identification and offset information to determine a position within the sequence. New patterns are constructed based on previous sequences and parameters via an iterative convolution method [p.58, Col. 1, Fig. 3, p.59, Col. 1], which shows generating updated instances of sequence by reference to previous parameters. New offset lists are generated [p.58, Col. 1]. The program obtains optimal patterns and performs pattern-based searches of databases, and displays discovered pattern results in

the form of sequences [p.56, Col. 1, and p.66, Col. 1 and Fig. 4, Table 2 and 4], which shows storing generated entries. Search results are tracked according to exact matches, matches within varying degrees of accuracy, and unmatched data [Table 5].

Rigoutsos does not teach deleting each matching subsequence from the sequence where it is found, as in claims 14, 27, and 28.

Rigoutsos does not teach concatenating unmatched regions of sequences that remain after deleting each matching subsequence to form and store a backbone sequence, as in claims 14, 24, and 27 (step vi).

Rigoutsos does not teach presenting sequences that include stored backbone sequence and at least one of the stored match-set data entries corresponding to the selected at least first one of the replets, as in claims 14, 24, and 27 (step viii).

Rigoutsos does not teach a first position parameter of each match-set entry denoting a location in the sequence and a second position parameter of each match-set entry denoting an offset position, and updating the first and second parameters of the entries in the match-set data structure to include the position of the selected at least first one of the replets, as in claims 14, 24, and 27 (step viii).

Rigoutsos does not teach generating or receiving a selection of a second one of the replets and x) the computer system generating and presenting a second instance of the sequence to a user responsive to at least second one of the replets and wherein the computer system performs the generating of the second instance of the sequence by reference to the updated first and second parameters for the second one of the replets, as in claims 14, 24, and 27 (steps ix and x).

Chen teaches a program for identifying repeats in long DNA sequences [Introduction]. In particular, the program performs a step for extracting repeats and concatenates regions (other that repeats) and sends the string as input to another program [p.1697, Col. 2, p.1698, Col. 1, and Fig. 1]. The program also performs encoding of repeat regions in the DNA sequences [p.1696-97, Methods]. A graphic interface is provided for searching a sequence database using user-defined parameters [Fig. 6].This program is beneficial for improving search results through sequence compression [Introduction].

Orcutt teaches a nucleic acid sequence database computer system and program [Fig. 1]. The user can extract and concatenate any of the stored sequences, the complement, or the protein translations [p.168]. Sequences can be stored and examined by other matching programs [p.168]. Orcutt teaches updating the information stored in the computer system by considering old data, adding new data, and deleting old data, where the data can include files codes, indexes, sequence information, etc. [p.168], which teaches a computer system capable of updating parameters after receiving a selection. Orcutt also teaches updating a sequence database containing match-set data [p.169]. The system contains print functions for displaying the contents of any file [p.165]. The system provides match functions for determining sequence matches and mismatches program, and outputs a representation of a sequence in response to a matching program that considers contiguous residues that match [p.164, last ¶, p.167]. The system will also search and identify non-exact matches [p.165], which meets claim language for non-selected replets.

UK CROPNET teaches a computer based method for graphically displaying sequences from a database. In particular, the generated displays include a combination of different sequence information including BLAST matches to an insert sequence, homology matches to an insert sequence, introns, exons, textual information [See pages 2-3]. Additionally, graphs are generated to include representations of physical positions of a probe in a region of a chromosome, backbone markers, and specific sequence information [p.4].

Zhang teaches a computer-based method for identifying and graphically displaying repeat regions on a gene [Abstract, Fig. 1]. The program also displays gaps, mismatches (i.e. non-matching) regions, gaps, and multiple alignments [Fig. 2, Fig. 3]. The program interface also allows for searching a database and using filtering commands [Fig. 6], which inherently functions to remove data from a viewable data set (i.e. deletion). The program is beneficial for creating user friendly interpretation for viewing results when matching database sequences [Abstract].

It would have been obvious to someone of ordinary skill in the art at the time of the instant invention to have deleted each matching subsequence from the sequence where it is found, in the method of Rigoutsos, with a reasonable expectation of success, since Chen and Orcutt teach programs for deleting repeats and concatenating any stored sequences, as set forth above. The motivation would have been to improve searching by reducing the amount of data for processing, as suggested by Orcutt [p.157], or through sequence compression, as shown by Chen [Introduction].

It would have been obvious to someone of ordinary skill in the art at the time of the instant invention to have generated sequences including backbone sequences and at

least one of the stored match-set data entries corresponding to the selected at least first one of the replets, in the method made obvious by Rigoutsos, Orcutt, and Chen, with a reasonable expectation of success, since UK CROPNET shows displaying sequences using a program that includes stored match-set data [See pages 2-3], as well as positional data and backbone sequences [p.4]. The motivation would have been to improve sequence analysis using a user friendly program for viewing results when matching database sequences, as suggested by Zhang.

It would have been obvious to someone of ordinary skill in the art at the time of the instant invention to have provided a predictable variation of the display of parameters, such as presenting a first position parameter of each match-set entry denoting a location in the sequence and a second position parameter of each match-set entry denoting an offset position, in the method made obvious by Rigoutsos, Orcutt, and Chen, with a reasonable expectation of success, since Rigoutsos teaches location and offset parameters and a parameter (Ls) denoting sequence matches at a specific offset; p.56, Col. 2, and in view of the rationale for a *prima facie* case of obviousness provided by the Supreme Court in *KSR International Co. v. Teleflex Inc.*, 550 U.S. 398 (2007). See MPEP 2143. In this case, the rationale would have been to improve the representation of known parameters (e.g. SEQ ID and offset) based on variations of known design incentives, such as combining known parameters into one coordinate-based parameter; e.g. (SEQ ID, offset), since these variations are predictable to one of ordinary skill in the art. For these reasons, the instant claims do not recite any new element or new function or unpredictable result.

It would have been obvious to someone of ordinary skill in the art at the time of the instant invention to have updated the first and second parameters of the entries in the match-set data structure to include the position of the selected replets, in the method made obvious by Rigoutsos, Orcutt, and Chen, with a reasonable expectation of success, since Rigoutsos shows generating new patterns (i.e. replets) and related parameters of position and offset; see p.58, Col. 1, which suggests updating first and second parameters of match-set data. The motivation would have been to generate a maximal patterns and detected non-maximal patterns with minimal effort, as suggested by Rigoutsos; p.58, Col. 2.

It would further have been obvious to have concatenated unmatched regions of sequences that remain after deleting each matching subsequence to form and store a backbone sequence, in the method made obvious by Rigoutsos, Chen, and Orcutt, with a reasonable expectation of success, since Orcutt provides software for displaying and updating unmatched data sets, as shown above, and since Zhang teaches a program for identifying and graphically displaying repeat mismatches (i.e. non-matching) regions, and multiple alignments, as set forth above. The motivation would have been to improve sequence analysis using a user friendly program for viewing results when matching database sequences, as set forth above Zhang.

It would have been obvious to someone of ordinary skill in the art at the time of the instant invention to have generated a second instance of a sequence by reference to the updated first and second parameters for the second one of the replets, in the method made obvious by Rigoutsos, Chen, Orcutt, and Zhang, with a reasonable expectation of success, since Rigoutsos provides an iterative method for obtaining optimal replets and

generating a plurality of sequence matches, as set forth above, and since Zhang shows that new sequences can be generated by filtering a database using user-defined parameters with predictable results, as set forth above, which suggests generating new sequences by reference to updated first and second parameters. The motivation would have been to improve sequence analysis using a user friendly program for viewing results when matching database sequences, as set forth above Zhang.

Claims 3-6, 10, 14-22, 24-28 are rejected under 35 U.S.C. 103(a) as being unpatentable over Rigoutsos et al. (Bioinformatics, 1998, Vol. 14, No. 1, p. 55-67), in view of Chen et al. (Bioinformatics, 2002, Vol. 18, No. 12, p.1696-1698), in view of Orcutt et al. (Nucleic Acids Research, 1982, Vol. 10, No. 1, p. 157-174), in view of Zhang et al. (Genome Research, 1997, Vol. 7, p.649-656), in view of UK CROPNETT (http://ukcrop.net/agr/sequence_display_key#sequence; Published 2001, p.1-5), and in view of Martinez et al. (Nucleic Acids Research, 1983, Vol. 11, No. 13, p. 4629-4634).

Rigoutsos, Chen, Orcutt, Zhang, and UK CROPNET make obvious the method, system, and computer readable medium of claims 4, 5, 14-22, 24, 27, and 28, as set forth above.

Rigoutsos, Chen, Orcutt, Zhang, and UK CROPNET do not teach storing information in a table using a "pointer", as in claims 3, 6, and 25.

Rigoutsos, Chen, Orcutt, Zhang, and UK CROPNET do not specifically teach storing multiple views of the sequence data at multiple levels of abstraction, as in claim 10. However, this limitation would have been obvious to one of ordinary skill in the art at

the time of the invention since both Zhang and UK CROPNET teach computer programs that are capable of graphically displaying sequence data comprising various types of data and since UK CROPNET teaches using different graphical schemes for distinguishing between the different types of data present (e.g. different colors), as set forth above, which reasonably suggests the claimed limitation. The motivation would have been to improve sequence analysis using a user friendly program for viewing results when matching database sequences, as set forth above Zhang.

Martinez teaches a computer program for finding repeats in molecular sequences using pointers to indicate order and variation between sequences [Abstract and p.4630].

It would have been obvious to someone of ordinary skill in the art at the time of the instant invention to have stored information in a table using a pointer, in the method, system, and computer readable media made obvious by Rigoutsos, Chen, Orcutt, Zhang, and UK CROPNET, with a reasonable expectation of success, since Martinez teaches a program that finds repeats in molecular sequences using pointers, as shown above. The motivation would have been to indicate order and variation between sequences, as shown by Martinez [p.4630, 4634].

Response to Arguments

Applicant's arguments filed 5/3/2010 have been fully considered but are not persuasive for the following reasons.

In response to applicant's arguments against the references individually, one cannot show nonobviousness by attacking references individually where the rejections are based on combinations of references. See In re Keller, 642 F.2d 413, 208 USPQ 871 (CCPA 1981); In re Merck & Co., 800 F.2d 1091, 231 USPQ 375 (Fed. Cir. 1986).

In response to applicant's assertion that Rigoutsos does not teach sequence identifier and offset information that comprises a first and second position parameter, Rigoutsos teaches an offset list comprising sequence matches at multiple offset positions; see p.56, Col. 2, which satisfies the claim language for a first and second position parameter.

In response to applicant's assertion that UK CROPNET does not teach or suggest updating, after receiving a replet selection, first and second parameters for any non-selected replet associated with the selected one of the replets, the claims do not recite this limitation.

In response to applicant's assertion that UK CROPNET does not teach or suggest updating first and second parameters after receiving a replet selection, where the updating is responsive to a position of the selected one of the replets, UK CROPNET was not cited as a teaching for this limitation. UK CROPNET was cited as a teaching for a computer system for generating and presenting multiple instances of sequences to a user. The graphical presentation includes a combination of information including matches to an insert sequence, sequence position, and textual information [See pages 2-3], as set forth above.

Conclusion

No claims are allowed.

THIS ACTION IS MADE FINAL. Applicant is reminded of the extension of time policy as set forth in 37 CFR 1.136(a).

A shortened statutory period for reply to this final action is set to expire THREE MONTHS from the mailing date of this action. In the event a first reply is filed within

TWO MONTHS of the mailing date of this final action and the advisory action is not mailed until after the end of the THREE-MONTH shortened statutory period, then the shortened statutory period will expire on the date the advisory action is mailed, and any extension fee pursuant to 37 CFR 1.136(a) will be calculated from the mailing date of the advisory action. In no event, however, will the statutory period for reply expire later than SIX MONTHS from the mailing date of this final action.

Any inquiry concerning this communication or earlier communications from the examiner should be directed to Pablo Whaley whose telephone number is (571)272-4425. The examiner can normally be reached between 12pm-8pm.

If attempts to reach the examiner by telephone are unsuccessful, the examiner's supervisor, Marjorie Moran can be reached at 571-272-0720. The fax phone number for the organization where this application or proceeding is assigned is 571-273-8300.

Information regarding the status of an application may be obtained from the Patent Application Information Retrieval (PAIR) system. Status information for published applications may be obtained from either Private PAIR or Public PAIR. Status information for unpublished applications is available through Private PAIR only. For more information about the PAIR system, see http://pair-direct.uspto.gov. Should you have questions on access to the Private PAIR system, contact the Electronic Business Center (EBC) at 866-217-9197 (toll-free).

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